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RAW SEQUENCE LISTING

DATE: 07/23/2002

PATENT APPLICATION: US/09/981,397A

TIME: 15:12:40

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\07232002\I981397A.raw

3 <110> APPLICANT: Axxima Pharmaceuticals AG
 4 Schubart, Daniel
 5 Habenberger, Peter
 6 Stein-Gerlach, Matthias
 7 Bevec, Dorian
 9 <120> TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and
 their
 10 Inhibition
 12 <130> FILE REFERENCE: AXM-004.1 US
 14 <140> CURRENT APPLICATION NUMBER: 09/981,397A
 C--> 15 <141> CURRENT FILING DATE: 2002-06-28
 17 <150> PRIOR APPLICATION NUMBER: 60/240,750
 18 <151> PRIOR FILING DATE: 2000-10-16
 20 <160> NUMBER OF SEQ ID NOS: 22
 22 <170> SOFTWARE: PatentIn version 3.1
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 25 <211> LENGTH: 18
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: synthetic polyT primer
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 33 <221> NAME/KEY: misc_feature
 34 <222> LOCATION: (18)..(18)
 35 <223> OTHER INFORMATION: n = a,c,g or t
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 39 <221> NAME/KEY: misc_feature
 40 <222> LOCATION: (17)..(17)
 41 <223> OTHER INFORMATION: v = a,g or c
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 49 <211> LENGTH: 28
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: cDNA probe for NIK-interacting kinase
 56 <400> SEQUENCE: 2
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 60 <210> SEQ ID NO: 3
 61 <211> LENGTH: 30
 62 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial Sequence
 65 <220> FEATURE:

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66 <223> OTHER INFORMATION: cDNA probe for cellular protein RIP
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69 gtgctcaatg cagttgggcc ccttgtacac 30
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73 <211> LENGTH: 27
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: cDNA probe for cellular protein kinase RICK
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81 gtcgagcagc ggagtgtgga tgtgcag 27
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85 <211> LENGTH: 23
86 <212> TYPE: PRT
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: NIK peptide immunogen
92 <400> SEQUENCE: 5
94 Cys Asn Pro Thr Asn Thr Arg Pro Gln Ser Asp Thr Pro Glu Ile Arg
95 1 5 10 15
98 Lys Tyr Lys Lys Arg Phe Asn
99 20
102 <210> SEQ ID NO: 6
103 <211> LENGTH: 34
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: loxP sequence for recombination vector
110 <400> SEQUENCE: 6
111 ataacttcgt atagcataca ttatacgaag ttat 34
114 <210> SEQ ID NO: 7
115 <211> LENGTH: 31
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
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122 <400> SEQUENCE: 7
123 gctcactagt ggcctagcct ggcctcatggc c 31
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128 <212> TYPE: DNA
129 <213> ORGANISM: Artificial Sequence
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132 <223> OTHER INFORMATION: primer US-10(198918)PacI
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138 <210> SEQ ID NO: 9
139 <211> LENGTH: 33
140 <212> TYPE: DNA

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141 <213> ORGANISM: Artificial Sequence
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144 <223> OTHER INFORMATION: primer US-9-3'PmeI
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152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: primer US-5'CLAI
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163 <211> LENGTH: 20
164 <212> TYPE: DNA
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168 <223> OTHER INFORMATION: primer US-9(198789)
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175 <211> LENGTH: 19
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: primer US-10(199100)
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186 <210> SEQ ID NO: 13
187 <211> LENGTH: 2501
188 <212> TYPE: DNA
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 13
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194 catccgggga atgggcgccc tcgtgacctc gtgttgccgg gcaaaaaggg tcttgccggc 120
196 ctgcgtcgtg caggggcgta tctgggcgcc tgagcgcgca gtgggagcct tgggagccgc 180
198 cgcagcaggg ggcacacccg gaaccggcct gagcgcgccg gaccatgaac ggggaggcca 240
200 tctgcagcgc cctgcccacc attccctacc acaaactcgc cgacctgcgc tacctgagcc 300
202 gcggcgccctc tggcactgtg tcgtccgccc gccacgcaga ctggcgcgtc caggtggccg 360
204 tgaagcacct gcacatccac actccgctgc tcgacagtga aagaaaggat gtcttaagag 420
206 aagctgaaat ttacacaaa gctagattta gttacattct tccaattttg ggaatttgca 480
208 atgagccctga atttttgagg atagtactg aatacatgcc aaatggatca ttaaataaac 540
210 tcctacatag gaaaactgaa tatcctgatg ttgcttgccc attgagattt cgcacacctg 600
212 atgaaattgc ccttggtgta aattacctgc acaatatgac tcctccttta cttcatcatg 660
214 acttgaagac tcagaatatc ttattggaca atgaatttca tgtaagatt gcagattttg 720
216 gtttatcaaa gtggcgcatg atgtccctct cacagtcacg aagtagcaaa tctgcaccag 780
218 aaggaggggac aattatctat atgcccactg aaaactatga acctggacaa aaatcaaggg 840
220 ccagtatcaa gcacgatata tatagctatg cagttatcac atgggaagtg ttatccagaa 900

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222 aacagccttt tgaagatgtc accaatcctt tgcagataat gtatagtgtg tcacaaggac 960
224 atcgacctgt tattaatgaa gaaagtttgc catatgatat acctcaccga gcacgtatga 1020
226 totctctaata agaaagtggg tgggcacaaa atccagatga aagaccatct ttcttaaaat 1080
228 gtttaataga acttgaacca gttttgagaa catttgaaga gataactttt cttgaagctg 1140
230 ttattcagct aaagaaaaca aagttacaga gtgtttcaag tgccattcac ctatgtgaca 1200
232 agaagaaaat ggaattatct ctgaacatac ctgtaaatca tgggtccaca gaggaatcat 1260
234 gtggatcctc tcagctccat gaaaatagtg gttctcctga aacttcaagg tccctgccag 1320
236 ctcccaaga caatgatatt ttatctagaa aagctcaaga ctgttatttt atgaagctgc 1380
238 atcactgtcc tggaaatcac agttgggata gcaccatttc tggttctcaa agggctgcat 1440
240 tctgtgatca caagaccact ccatgtcttt cagcaataat aaatccactc tcaactgcag 1500
242 gaaactcaga acgtctgcag cctgggtatag ccagcagtg gatccagagc aaaagggaag 1560
244 acattgtgaa ccaaatgaca gaagcctgcc ttaaccagtc gctagatgcc cttctgtcca 1620
246 gggacttgat catgaaagag gactatgaac ttgttagtac caagcctaca aggacctcaa 1680
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250 tacaaaaatt gaaagataac aaacaaatgg gtcttcagcc ttaccgggaa atacttgtgg 1800
252 tttctagatc accatcttta aatttacttc aaaataaaaag catgtaagtg actgtttttc 1860
254 aagaagaaat gtgtttcata aaaggatatt tatactctctg ttgctttgac tttttttata 1920
256 taaaatccgt gagtattaaa gctttattga aggttctttg ggtaaatatt agtctccctc 1980
258 catgacactg cagtattttt tttaattaat acaagtaaaa agttgaattt ggttgaattt 2040
260 gctacatagt tcaattttta tgtctctttt gttaacagaa accactttta aaggatagta 2100
262 attattcttg tttataacag tgccttaagg tatgatgtat ttctgatgga agccattttc 2160
264 acattcatgt tcttcatgga ttatttgtaa cttgtctaag atgcaatttg attttatgaa 2220
266 gtatataccc tttaccacc agagacagta cagaatccct gccctaaaat ccaggctta 2280
268 attgcccctac aaagggttat taatttaaaa ctccattatt aggtattcat tttaaagttt 2340
270 tatttatgaa ttccctttaa aaatgatatt tcaaaggtaa aacaatacaa tataaagaaa 2400
272 aaaataaata tattaatacc ggcttctgtt ccccatTTTT aacctcagcc ttccctactg 2460
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277 <210> SEQ ID NO: 14

278 <211> LENGTH: 540

279 <212> TYPE: PRT

280 <213> ORGANISM: Homo sapiens

282 <400> SEQUENCE: 14

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288 Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
289 20 25 30
292 Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
293 35 40 45
296 Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu
297 50 55 60
300 Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Leu Pro
301 65 70 75 80
304 Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu
305 85 90 95
308 Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu
309 100 105 110
312 Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile
313 115 120 125
316 Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His

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317      130      135      140
320 His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val
321 145      150      155      160
324 Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser
325      165      170      175
328 Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr
329      180      185      190
332 Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile
333      195      200      205
336 Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser
337      210      215      220
340 Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr
341 225      230      235      240
344 Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro
345      245      250      255
348 Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly
349      260      265      270
352 Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile
353      275      280      285
356 Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu
357      290      295      300
360 Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala
361 305      310      315      320
364 Ile His Leu Cys Asp Lys Lys Lys Met Glu Leu Ser Leu Asn Ile Pro
365      325      330      335
368 Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His
369      340      345      350
372 Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln
373      355      360      365
376 Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys
377      370      375      380
380 Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly
381 385      390      395      400
384 Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr Pro Cys Ser Ser
385      405      410      415
388 Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln
389      420      425      430
392 Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val
393      435      440      445
396 Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu
397      450      455      460
400 Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys
401 465      470      475      480
404 Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile
405      485      490      495
408 Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn
409      500      505      510
412 Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg
413      515      520      525

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 18

Seq#:15; N Pos. 2141,2311,2452,2496